

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/155,676ADATE: 04/22/2000  
TIME: 01:05:44

INPUT SET: S35359.raw

#13

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

## (1) General Information:

(i) APPLICANT: WALLACH, David  
MALININ, Nikolai  
BOLDIN, Mark  
KOVALENKO, Andrei  
METT, Igor

(ii) TITLE OF INVENTION: MODULATORS OF TNF RECEPTOR ASSOCIATED  
FACTOR (TRAF), THEIR PREPARATION AND USE

(iii) NUMBER OF SEQUENCES: 20

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: BROWDY AND NEIMAR, P.L.L.C.  
(B) STREET: 624 Ninth Street, N.W., Suite 300  
(C) CITY: Washington  
(D) STATE: D.C.  
(E) COUNTRY: USA  
(F) ZIP: 20001

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/155,676  
(B) FILING DATE: 04-JAN-1999  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/IL97/00117  
(B) FILING DATE: 01-APR-1997

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: IL 117800  
(B) FILING DATE: 02-APR-1996

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: IL 119133  
(B) FILING DATE: 26-AUG-1996

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47 (viii) ATTORNEY/AGENT INFORMATION:  
48 (A) NAME: BROWDY, Roger L.  
49 (B) REGISTRATION NUMBER: 25,618  
50 (C) REFERENCE/DOCKET NUMBER: WALLACH=21  
51  
52 (ix) TELECOMMUNICATION INFORMATION:  
53 (A) TELEPHONE: 202-628-5197  
54 (B) TELEFAX: 202-737-3528  
55  
56  
57 (2) INFORMATION FOR SEQ ID NO: 1:  
58  
59 (i) SEQUENCE CHARACTERISTICS:  
60 (A) LENGTH: 1906 base pairs  
61 (B) TYPE: nucleic acid  
62 (C) STRANDEDNESS: single  
63 (D) TOPOLOGY: linear  
64  
65 (ii) MOLECULE TYPE: cDNA  
66  
67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
68  
69 CATTGGGTCA CGCGGTGGCG GCGCTCTAGA ATAGTGGATC CCCCAGGGCTG CAGGAATTCTG 60  
70  
71 ATTCGAGGCC ACGAAGGCCG GCGGCGCGGC GCANGCACCG GCCCGGGGAN AGGCNCCATG 120  
72  
73 AGCGGATCNC NGAACNATGA CAAAAGACAA TTTCTGCTGG AGCGACTGCT GGATGCAGTG 180  
74  
75 AAACAGTGCC AGATCCGCTT TNGAGGGAGA AAGGAGATTG CCTCGGATTC CGACAGCAGG 240  
76  
77 GTCACCTGTC TGTGTGCCCA GTTTGAAGCC GTCCTGCAGC ATGGCTTGAA GAGGAGTCGA 300  
78  
79 GGATTGGCAC TCACAGCGGC AGCGATCAAG CAGGCAGCGG GCTTTGCCAG CAAAACCGAA 360  
80  
81 ACAGAGCCCG TGTTCTGGTA CTACGTGAAG GAGGTCCTCA ACAAGCACGA GCTGCAGCGC 420  
82  
83 TTCTACTCCC TGCGCCACAT CGCCTCAGAC GTGGGCCGGG GTCGCGCCTG GCTGCGCTGT 480  
84  
85 GCCCTCAACG AACACTCCCT GGAGCGCTAC CTGCACATGC TCCTGGCCGA CCGCTGCAGG 540  
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87 CTGAGCACTT TTTATGAAGA CTGGTCTTTT GTGATGGATG AAGAAAGGTC CAGTATGCTT 600  
88  
89 CCTACCATGG CAGCAGGTCT GAACTCCATA CTCTTTGCCA TTAACATCGA CAACAAGGAT 660  
90  
91 TTGAACGGGC AGAGTAAGTT TGCTCCACC GTTTCAGACC TCTTAAAGGA GTCAACGCAG 720  
92  
93 AACGTGACCT CCTTGCTGAA GGAGTCCAG CAAGGAGTGA GCAGCCTGTT CAGGGAGATC 780  
94  
95 ACAGCCTCCT CTGCCGTCTC CATCCTCATC AAACCTGAAC AGGAGACCGA CCCTTGCCCTG 840  
96  
97 TCGTGTCCAG GAATGTCAGT GCTGATGCCA AATGCAAAAA GGAGCGGAAG AAGAAAAAGA 900  
98  
99 AAGTGACCAA CATAATCTCA TTTGATGATG AGGAAGATGA GCAGAACTCT GGGGACGTGT 960

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101 TTAAAAAGAC ACCTGGGGCA GGGGAGAGCT CAGAGGACAA CTCCGACCGC TCCTCTGTCA 1020
102
103 ATATCATGTC CGCCTTTGAA AGCCCCCTTCG GGCCTAACTC CAATGGAATC AGAGCAGCAA 1080
104
105 CTCATGGAAA ATTGATTCCC TGTCTTTGAA CGGGGAGTTT GGGTACCAGA AGCTTGATGT 1140
106
107 GAAAAGCATC GATGATGAAG ATGTGGATGA AAACGAAGAT GACGTGTATG GAAACTCATC 1200
108
109 AGGAAGGAAG CACAGGGGCC ACTCGGAGTC GCCCGAGAAG CCACTGGAAG GGAACACCTG 1260
110
111 CCTCTCCCAG ATGCACAGCT GGGCTCCGCT GAAGGTGCTG CACAATGACT CCGACATCCT 1320
112
113 CTTCCCTGTC AGTGGCGTGG GCTCCTACAG CCCAGCAGAT GCCCCCTCG GAAGCCTGGA 1380
114
115 GAACGGGACA GGACCAGAGG ACCACGTTCT CCCGGATCCT GGACTTCGGT ACAGTGTGGA 1440
116
117 AGCCAGCTCT CCAGGCCACG GAAGTCCTCT GAGCAGCCTG TTACTTCTGC CTCAGTGCCA 1500
118
119 GAGTCCATGA CAATTAGTGA ACTGCGCCAG GCCACTGTGG CCATGATGAA CAGGAAGGAT 1560
120
121 GAGCTGGAGG AGGAGAACAG ATCACTGCGA AACCTGCTCG ACGGTGAGAT GGAGCACTCA 1620
122
123 GCCGCGCTCC GGCAAGAGGT GGACACCTTG AAAAGGAAGG TGGCTGAACA GGAGGAGCGG 1680
124
125 CAGGGCATGA AGGTCCAGGC GCTGGCCAGC TATCTTTGCT ATTTTGTGAG GAGATTCTAA 1740
126
127 CCCCACGTGA GAACCATGTG GTGGAGAAAT GGAGGGAGAG AGAAATCCAA CAGTTCCTGA 1800
128
129 TAGTCTCATT TGAGCTCCTG GATCCAGTCT TTCCTGAAGC TGTGTTTCCT CTGGACTTTT 1860
130
131 CATGTATGTG AGCCAATAAA TTGCTTTCAT TCCTTGAAAA AAAAAA 1906
132

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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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145 Xaa Thr Gly Pro Gly Xaa Gly Xaa Met Ser Gly Ser Xaa Asn Xaa Asp
146 1          5          10          15
147
148 Lys Arg Gln Phe Leu Leu Glu Arg Leu Leu Asp Ala Val Lys Gln Cys
149          20          25          30
150
151 Gln Ile Arg Phe Xaa Gly Arg Lys Glu Ile Ala Ser Asp Ser Asp Ser
152          35          40          45

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153																			
154	Arg	Val	Thr	Cys	Leu	Cys	Ala	Gln	Phe	Glu	Ala	Val	Leu	Gln	His	Gly			
155		50					55					60							
156																			
157	Leu	Lys	Arg	Ser	Arg	Gly	Leu	Ala	Leu	Thr	Ala	Ala	Ala	Ile	Lys	Gln			
158	65					70					75					80			
159																			
160	Ala	Ala	Gly	Phe	Ala	Ser	Lys	Thr	Glu	Thr	Glu	Pro	Val	Phe	Trp	Tyr			
161					85					90					95				
162																			
163	Tyr	Val	Lys	Glu	Val	Leu	Asn	Lys	His	Glu	Leu	Gln	Arg	Phe	Tyr	Ser			
164				100					105					110					
165																			
166	Leu	Arg	His	Ile	Ala	Ser	Asp	Val	Gly	Arg	Gly	Arg	Ala	Trp	Leu	Arg			
167			115					120					125						
168																			
169	Cys	Ala	Leu	Asn	Glu	His	Ser	Leu	Glu	Arg	Tyr	Leu	His	Met	Leu	Leu			
170		130					135					140							
171																			
172	Ala	Asp	Arg	Cys	Arg	Leu	Ser	Thr	Phe	Tyr	Glu	Asp	Trp	Ser	Phe	Val			
173	145					150					155					160			
174																			
175	Met	Asp	Glu	Glu	Arg	Ser	Ser	Met	Leu	Pro	Thr	Met	Ala	Ala	Gly	Leu			
176					165					170					175				
177																			
178	Asn	Ser	Ile	Leu	Phe	Ala	Ile	Asn	Ile	Asp	Asn	Lys	Asp	Leu	Asn	Gly			
179				180					185					190					
180																			
181	Gln	Ser	Lys	Phe	Ala	Pro	Thr	Val	Ser	Asp	Leu	Leu	Lys	Glu	Ser	Thr			
182			195					200					205						
183																			
184	Gln	Asn	Val	Thr	Ser	Leu	Leu	Lys	Glu	Ser	Thr	Gln	Gly	Val	Ser	Ser			
185		210					215					220							
186																			
187	Leu	Phe	Arg	Glu	Ile	Thr	Ala	Ser	Ser	Ala	Val	Ser	Ile	Leu	Ile	Lys			
188	225					230					235					240			
189																			
190	Pro	Glu	Gln	Glu	Thr	Asp	Pro	Cys	Leu	Ser	Cys	Pro	Gly	Met	Ser	Val			
191					245					250					255				
192																			
193	Leu	Met	Pro	Asn	Ala	Lys	Arg	Ser	Gly	Arg	Arg	Lys	Arg	Lys	Xaa	Pro			
194				260					265					270					
195																			
196	Thr	Xaa	Ser	His	Leu	Met	Met	Arg	Lys	Met	Ser	Arg	Thr	Leu	Gly	Thr			
197			275					280					285						
198																			
199	Cys	Leu	Lys	Arg	His	Leu	Gly	Gln	Gly	Arg	Ala	Gln	Arg	Thr	Thr	Pro			
200		290					295					300							
201																			
202	Thr	Ala	Pro	Leu	Ser	Ile	Ser	Cys	Pro	Pro	Leu	Lys	Ala	Pro	Ser	Gly			
203	305					310					315					320			
204																			
205	Leu	Thr	Pro	Met	Glu	Ser	Glu	Gln	Gln	Leu	Met	Glu	Asn	Xaa	Phe	Pro			

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206		325		330		335
207						
208	Val Phe Glu Arg Gly Val Trp Val Pro Glu Ala Xaa Cys Glu Lys His					
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210						
211	Arg Xaa Xaa Arg Cys Gly Xaa Lys Arg Arg Xaa Arg Val Trp Lys Leu					
212		355		360		365
213						
214	Ile Arg Lys Glu Ala Gln Gly Pro Leu Gly Val Ala Arg Glu Ala Thr					
215		370		375		380
216						
217	Gly Arg Glu His Leu Pro Leu Pro Asp Ala Gln Leu Gly Ser Ala Glu					
218		385		390		395
219						400
220	Gly Ala Ala Gln Xaa Leu Arg His Pro Leu Pro Cys Gln Trp Arg Gly					
221		405		410		415
222						
223	Leu Leu Gln Pro Ser Arg Cys Pro Pro Arg Lys Pro Gly Glu Arg Asp					
224		420		425		430
225						
226	Arg Thr Arg Gly Pro Arg Ser Pro Gly Ser Trp Thr Ser Val Gln Cys					
227		435		440		445
228						
229	Gly Ser Gln Leu Ser Arg Pro Arg Lys Ser Ser Glu Gln Pro Val Thr					
230		450		455		460
231						
232	Ser Ala Ser Val Pro Glu Ser Met Thr Ile Ser Glu Leu Arg Gln Ala					
233		465		470		475
234						480
235	Thr Val Ala Met Met Asn Arg Lys Asp Glu Leu Glu Glu Glu Asn Arg					
236		485		490		495
237						
238	Ser Leu Arg Asn Leu Leu Asp Gly Glu Met Glu His Ser Ala Ala Leu					
239		500		505		510
240						
241	Arg Gln Glu Val Asp Thr Leu Lys Arg Lys Val Ala Glu Gln Glu Glu					
242		515		520		525
243						
244	Arg Gln Gly Met Lys Val Gln Ala Leu Ala Ser Tyr Leu Cys Tyr Phe					
245		530		535		540
246						
247	Val Arg Arg Phe Xaa Pro His Val Arg Thr Met Trp Trp Arg Asn Gly					
248		545		550		555
249						560
250	Gly Arg Glu Lys Ser Asn Ser Ser Xaa Xaa Ser His Leu Ser Ser Trp					
251		565		570		575
252						
253	Ile Gln Ser Phe Leu Lys Leu Cys Phe Leu Trp Thr Phe His Val Cys					
254		580		585		590
255						
256	Glu Pro Ile Asn Cys Phe His Ser Leu Lys Lys Lys					
257		595		600		
258						

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/155,676A**

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